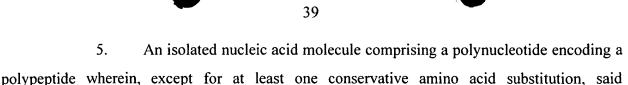
CLAIMS

We claim:

- 1. An isolated nucleic acid molecule comprising a polynucleotide selected from the group consisting of:
- (a) a polynucleotide encoding amino acids from about 1 to about 273 of SEQ ID NO:2;
- (b) a polynucleotide encoding amino acids from about 2 to about 273 of SEQ ID NO:2;
- (c) a polynucleotide encoding amino acids from about 26 to about 273 of SEQ ID NO:2;
- (d) the polynucleotide complement of the polynucleotide of (a), (b), or (c); and
- (e) a polynucleotide at least 90% identical to the polynucleotide of (a), (b), (c), or (d).
- 2. An isolated nucleic acid molecule comprising 24-738 contiguous nucleotides from the coding region of SEQ ID NO:1.
- 3. The isolated nucleic acid molecule of claim 2, which comprises 50-500 contiguous nucleotides from the coding region of SEQ ID NO:1.
- 4. The isolated nucleic acid molecule of claim 3, which comprises 75-250 contiguous nucleotides from the coding region of SEQ ID NO:1.



- (a) amino acids about 1 to about 273 of SEQ ID NO:2;
- (b) amino acids about 2 to about 273 of SEQ ID NO:2; and
- (c) amino acids 26 to 273 of SEQ ID NO:2.

polypeptide has an amino acid sequence selected from the group consisting of:

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- 6. The isolated nucleic acid molecule of claim 1, which is DNA.
- 7. A method of making a recombinant vector comprising inserting a nucleic acid molecule of claim 1 into a vector in operable linkage to a promoter.
 - 8. A recombinant vector produced by the method of claim 7.
- 9. A method of making a recombinant host cell comprising introducing the recombinant vector of claim 8 into a host cell.
 - 10. A recombinant host cell produced by the method of claim 9.
- 11. A recombinant method of producing a polypeptide, comprising culturing the recombinant host cell of claim 10 under conditions such that said polypeptide is expressed and recovering said polypeptide.
- 12. An isolated polypeptide comprising amino acids at least 95% identical to amino acids selected from the group consisting of:
 - (a) amino acids about 1 to about 273 of SEQ ID NO:2;
 - (b) amino acids about 2 to about 273 of SEQ ID NO:2; and
 - amino acids 26 to 273 of SEQ ID NO:2. (c)





- 13. An isolated polypeptide wherein, except for at least one conservative amino acid substitution, said polypeptide has an amino acid sequence selected from the group consisting of:
 - (a) amino acids about 1 to about 273 of SEQ ID NO:2;
 - (b) amino acids about 2 to about 273 of SEQ ID NO:2; and
 - (c) amino acids 26 to 273 of SEQ ID NO:2.
- 14. An isolated polypeptide comprising amino acids selected from the group consisting of:
 - (a) amino acids about 1 to about 273 of SEQ ID NO:2;
 - (b) amino acids about 2 to about 273 of SEQ ID NO:2; and
 - (c) amino acids 26 to 273 of SEQ ID NO:2.
 - 15. An epitope-bearing portion of the polypeptide of SEQ ID NO:2.
- 16. The epitope-bearing portion of claim 15, which comprises 8-25 contiguous amino acids of SEQ ID NO:2.
- 17. The epitope-bearing portion of claim 15, which comprises 10 contiguous amino acids of SEQ ID NO:2.
 - 18. An isolated antibody that binds specifically to the polypeptide of claim 12.
 - 19. An isolated antibody that binds specifically to a polypeptide of claim 13.
 - 20. An isolated antibody that binds specifically to the polypeptide of claim 14.
- 21. A method for detecting a human gene encoding SEQ ID NO:2 said method comprising obtaining in computer-readable format SEQ ID NO:1, comparing said sequence with



polynucleotide sequences of a human genome, and identifying one or more human genome sequences having at least 95% sequence identity to SEQ ID NO:1 as determined by the Smith-Waterman algorithm using an affine gap search with a gap open penalty of 12 and a gap extension penalty of 1 as parameters.

- 22. A non-naturally occurring fusion protein comprising a first protein segment and a second protein segment fused to each other by means of a peptide bond, wherein the first protein segment comprises at least six contiguous amino acids selected from an amino acid sequence encoded by the nucleotide sequence of SEQ ID NO:1 or the complement thereof.
- 23. The fusion protein of claim 22 wherein said first protein segment comprises at least six contiguous amino acids of SEQ ID NO:2.
- The fusion protein of claim 23 wherein said first protein segment 24. comprises at least twelve contiguous amino acids of SEO ID NO:2.
- 25. The fusion protein of claim 22 wherein said first protein segment comprises amino acids 20-30 of SEQ ID NO:2.
- 26. The fusion protein of claim 24 wherein said first protein segment comprises at least 50 contiguous amino acids of SEQ ID NO:2.
- 27. The fusion protein of claim 26 wherein said first protein segment comprises at least 100 contiguous amino acids of SEO ID NO:2.
- 28. The fusion protein of claim 22 wherein said first protein segment comprises amino acids 26-287 of SEQ ID NO:2.



29. A method for comparing metastatic potential of tumor cells in a first and second tissue sample, comprising:

measuring in said tissue samples an expression product of a gene which comprises a polypeptide coding region of SEQ ID NO:1, wherein at least a two-fold greater expression of the product in the first tissue sample indicates a greater metastatic potential compared to the second tissue sample.

- 30. The method of claim 29 wherein the expression product is protein.
- 31. The method of claim 30 wherein the protein is measured using an antibody which specifically binds to the protein.
 - 32. The method of claim 29 wherein the expression product is mRNA.
- 33. The method of claim 32 wherein said mRNA is measured using a polynucleotide probe comprising at least 20 contiguous nucleotides of nucleotides 365-1173 of SEQ ID NO:1.
 - 34. A composition for inhibiting expression of protein by a mammary carcinoma cell, said composition comprising the polynucleotide of SEQ ID NO:4.
 - 35. A method of inhibiting expression of a protein by a mammary carcinoma cell, said method comprising contacting said cell with a composition comprising the polynucleotide of SEQ ID NO:4.